RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/718,952 A_
Source: _/Fw/6,_
Date Processed by STIC: _1/19/06_

ENTERED

IFW16

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 3 <110> APPLICANT: Hitz, William
 4        Sebastian, Scott
 5        Grace, John
 6        Streit, Leon
 8 <120> TITLE OF INVENTION: SOYBEAN PLANT PRODUCING SEEDS WITH REDUCED LEVELS OF
RAFFINOSE
 9        SACCHARIDES AND PHYTIC ACID
11 <130> FILE REFERENCE: BB1077 US DIV
13 <140> CURRENT APPLICATION NUMBER: 10/718,952A
14 <141> CURRENT FILING DATE: 2003-11-21
16 <150> PRIOR APPLICATION NUMBER: 10/025,003
17 <151> PRIOR FILING DATE: 2002-03-11
19 <150> PRIOR APPLICATION NUMBER: 09/299,315
20 <151> PRIOR FILING DATE: 1999-04-26
22 <150> PRIOR APPLICATION NUMBER: PCT/US98/06822
23 <151> PRIOR FILING DATE: 1998-04-07
25 <150> PRIOR APPLICATION NUMBER: 08/835,751
26 <151> PRIOR FILING DATE: 1997-04-08
28 <160> NUMBER OF SEQ ID NOS: 20
30 <170> SOFTWARE: Microsoft Office 97
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33 <211> LENGTH: 1760
34 <212> TYPE: DNA
35 <213> ORGANISM: Glycine max
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40 tgtacaacta cgaaaccacc gaacttgttc acgagaacag gaatggcacc tatcagtgga  180
41 ttgtcaaacc caaatctgtc aaatacgaat ttaaaaccaa catccatgtt cctaaattag  240
42 gggtaatgct tgtgggttgg ggtggaaaca acggctcaac cctcaccggt ggtgttattg  300
43 ctaaccgaga gggcatttca tgggctacaa aggacaagat tcaacaagcc aattactttg  360
44 gctccctcac ccaagcctca gctatccgag ttgggtcctt ccagggagag gaaatctatg  420
45 ccccattcaa gagcctgctt ccaatggtta accctgacga cattgtgttt ggggggatggg  480
46 atatcagcaa catgaacctg gctgatgcca tggccagggc aaaggtgttt gacatcgatt  540
47 tgcagaagca gttgaggcct tacatggaat ccatgcttcc actccccgga atctatgacc  600
48 cggatttcat tgctgccaac caagaggagc gtgccaacaa cgtcatcaag ggcacaaagc  660
49 aagagcaagt tcaacaaatc atcaaagaca tcaaggcgtt taaggaagcc accaaagtgg  720
50 acaaggtggt tgtactgtgg actgccaaca cagagaggta cagtaatttg gttgtgggcc  780
51 ttaatgacac catggagaat ctcttggctg ctgtggacag aaatgaggct gagatttctc  840
52 cttccacctt gtatgccatt gcttgtgtta tggaaaatgt tcctttcatt aatggaagcc  900
53 ctcagaacac ttttgtacca gggctgattg atcttgccat cgcgaggaac actttgattg  960
54 gtggagatga cttcaagagt ggtcagacca aaatgaaatc tgtgttggtt gatttccttg 1020
55 tggggctgg tatcaagcca acatctatag tcagttacaa ccatctggga acaatgatg 1080
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RAW SEQUENCE LISTING   DATE: 01/19/2006
PATENT APPLICATION: US/10/718,952A   TIME: 12:52:09

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62 tcagctacct caccaaggct cctctggttc caccgggtac accagtggtg aatgcattgt 1500
63 caaagcagcg tgcaatgctg gaaaacataa tgagggcttg tgttggattg ccccagaga 1560
64 ataacatgat tctcgagtac aagtgaagca tgggaccgaa gaataatata gttggggtag 1620
65 cctagctgaa tgttttatgt taataatatg tttgcttata attttgcaag tgtaattgaa 1680
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72 <213> ORGANISM: Glycine max
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79              20                  25                  30
81 His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
82          35                  40                  45
84 Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val
85      50                  55                  60
87 Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
88  65                  70                  75                  80
90 Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
91                  85                  90                  95
93 Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
94              100                 105                 110
96 Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
97              115                 120                 125
99 Leu Pro Met Val Asn Pro Asp Asp Ile Val Phe Gly Gly Trp Asp Ile
100     130                 135                 140
102 Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
103 145                 150                 155                 160
105 Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro
106                 165                 170                 175
108 Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
109             180                 185                 190
111 Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
112         195                 200                 205
114 Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
115     210                 215                 220
117 Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
118 225                 230                 235                 240
120 Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
121                 245                 250                 255
123 Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
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130     290             295             300
132 Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
133 305             310             315             320
135 Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
136         325             330             335
138 His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
139         340             345             350
141 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
142         355             360             365
144 Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
145     370             375             380
147 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Lys Arg Ala Met Asp
148 385             390             395             400
150 Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu
151         405             410             415
153 His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
154         420             425             430
156 Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Phe Lys Ala Glu
157         435             440             445
159 Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
160     450             455             460  .
162 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
163 465             470             475             480
165 Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
166         485             490             495
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176 <220> FEATURE:
177 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
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183 <211> LENGTH: 39
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic oligonuclotide
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196 <213> ORGANISM: Glycine max
198 <400> SEQUENCE: 5
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201 cagtggattg tcaaacccaa atctgtcaaa tacgaattta aaaccaacat ccatgttcct  180
202 aaattagggg taatgcttgt gggttggggt ggaaacaacg gctcaaccct caccggtggt  240
203 gttattgcta accgagaggg catttcatgg gctacaaagg acaagattca acaagccaat  300
204 tactttggct ccctcaccca agcctcagct atccgagttg ggtccttcca gggagaggaa  360
205 atctatgccc cattcaagag cctgcttcca atggttaacc ctgacgacat tgtgtttggg  420
206 ggatgggata tcagcaacat gaacctggct gatgccatgg ccagggcaaa ggtgtttgac  480
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208 tatgacccgg atttcattgc tgccaaccaa gaggagcgtg ccaacaacgt catcaagggc  600
209 acaaagcaag agcaagttca acaaatcatc aaagacatca aggcgtttaa ggaagccacc  660
210 aaagtggaca aggtggttgt actgtggact gccaacacag agaggtacag taatttggtt  720
211 gtgggcctta atgacaccat ggagaatctc ttggctgctg tggacagaaa tgaggctgag  780
212 atttctcctt ccaccttgta tgccattgct tgtgttatgg aaaatgttcc tttcattaat  840
213 ggaagccctc agaacacttt tgtaccaggg ctgattgatc ttgccatcgc gaggaacact  900
214 ttgattggtg gagatgactt caagagtggt cagaccaaaa tgaaatctgt gttggttgat  960
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217 aacgttgttg atgatatggt caacagcaat gccatcctct atgagcctgg tgaacatcca 1140
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222 accatcctca gctacctcac caaggctcct ctggttccac cgggtacacc agtggtgaat 1440
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228 <212> TYPE: PRT
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236             20                  25                  30
238 His Glu Asn Arg Asn Gly Thr Tyr Gln Trp Ile Val Lys Pro Lys Ser
239         35                  40                  45
241 Val Lys Tyr Glu Phe Lys Thr Asn Ile His Val Pro Lys Leu Gly Val
242     50                  55                  60
244 Met Leu Val Gly Trp Gly Gly Asn Asn Gly Ser Thr Leu Thr Gly Gly
245 65              70                  75                  80
247 Val Ile Ala Asn Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Ile
248             85                  90                  95
250 Gln Gln Ala Asn Tyr Phe Gly Ser Leu Thr Gln Ala Ser Ala Ile Arg
251             100                 105                 110
253 Val Gly Ser Phe Gln Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
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257   130   135   140
259 Ser Asn Met Asn Leu Ala Asp Ala Met Ala Arg Ala Lys Val Phe Asp
260 145   150   155   160
262 Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Met Leu Pro
263   165   170   175
265 Leu Pro Gly Ile Tyr Asp Pro Asp Phe Ile Ala Ala Asn Gln Glu Glu
266   180   185   190
268 Arg Ala Asn Asn Val Ile Lys Gly Thr Lys Gln Glu Gln Val Gln Gln
269   195   200   205
271 Ile Ile Lys Asp Ile Lys Ala Phe Lys Glu Ala Thr Lys Val Asp Lys
272   210   215   220
274 Val Val Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Ser Asn Leu Val
275 225   230   235   240
277 Val Gly Leu Asn Asp Thr Met Glu Asn Leu Leu Ala Ala Val Asp Arg
278   245   250   255
280 Asn Glu Ala Glu Ile Ser Pro Ser Thr Leu Tyr Ala Ile Ala Cys Val
281   260   265   270
283 Met Glu Asn Val Pro Phe Ile Asn Gly Ser Pro Gln Asn Thr Phe Val
284   275   280   285
286 Pro Gly Leu Ile Asp Leu Ala Ile Ala Arg Asn Thr Leu Ile Gly Gly
287   290   295   300
289 Asp Asp Phe Lys Ser Gly Gln Thr Lys Met Lys Ser Val Leu Val Asp
290 305   310   315   320
292 Phe Leu Val Gly Ala Gly Ile Lys Pro Thr Ser Ile Val Ser Tyr Asn
293   325   330   335
295 His Leu Gly Asn Asn Asp Gly Met Asn Leu Ser Ala Pro Gln Thr Phe
296   340   345   350
298 Arg Ser Lys Glu Ile Ser Lys Ser Asn Val Val Asp Asp Met Val Asn
299   355   360   365
301 Ser Asn Ala Ile Leu Tyr Glu Pro Gly Glu His Pro Asp His Val Val
302   370   375   380
304 Val Ile Lys Tyr Val Pro Tyr Val Gly Asp Ser Asn Arg Ala Met Asp
305 385   390   395   400
307 Glu Tyr Thr Ser Glu Ile Phe Met Gly Gly Lys Ser Thr Ile Val Leu
308   405   410   415
310 His Asn Thr Cys Glu Asp Ser Leu Leu Ala Ala Pro Ile Ile Leu Asp
311   420   425   430
313 Leu Val Leu Leu Ala Glu Leu Ser Thr Arg Ile Glu Phe Lys Ala Glu
314   435   440   445
316 Asn Glu Gly Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
317   450   455   460
319 Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
320 465   470   475   480
322 Ala Leu Ser Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
323   485   490   495
325 Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
326   500   505   510

VERIFICATION SUMMARY   DATE: 01/19/2006
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